

#10

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> New nucleotide sequences which code for the luxS gene

<130> 000457 BT

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<160> 4

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (342)..(1610)

<223> luxS gene

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cgggtgcgttc gaccgcgggc atcgcgtcga tgggaaggcc gtcagtaatt acttcggggg 180

ctgcctcggg gttggtctct ggggttgctt caggttccgc cggggtacaa gcggtgagca 240

35

tgatggaagc agcgaggata gtaggtaatg tacgacgcac gcagtcaagc ctagatcgtg 300

tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356

Met Lys Lys Gly Asn
1 5

40

caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404

Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala

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45

tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452

Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro

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35

50

atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500

Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr

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45

50

55

ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548

Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu

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ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596

Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile

70

75

80

85

SubA1

5	gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu 90 95 100	644
10	cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr 105 110 115	692
15	gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly 120 125 130	740
20	gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr 135 140 145	788
25	gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile 150 155 160 165	836
30	gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn 170 175 180	884
35	gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp 185 190 195	932
40	acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser 200 205 210	980
45	gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala 215 220 225	1028
50	atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu 230 235 240 245	1076
55	agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser 250 255 260	1124
60	aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu 265 270 275	1172
65	ggg att aat ttt gtg att tct gtc gac ggt gat gtt cgc caa ctg ccc Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro 280 285 290	1220
70	atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly 295 300 305	1268

SubA1

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5  aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc 1316
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10  tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364
   Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
                               330                               335                               340

15  ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc 1412
   Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
                               345                               350                               355

20  ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt 1460
   Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val
                               360                               365                               370

25  ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg 1508
   Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
   375                               380                               385

30  ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
   Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
   390                               395                               400                               405

35  tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac 1604
   Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp
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40  gat gag taaggctaga ctaaagtaag attcatctgc tcatcgatac tcttgaaggc 1660
   Asp Glu

45  gcattttcat tcgaaacgaa gtgcgcatt gggaaggacc tagttcaaac aatgattcgc 1720
   gtgctgcttg ctgatgacca cgaaatcgtg aggctcggac tccgagctgt gctggaaagc 1780
   gccgaggaca ttgaagtggg gggcgaagtc tccaccgccg aaggtgcggt gcaggcagcc 1840
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55  Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
     35 40 45
     Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
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5 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
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 10 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
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 15 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 100 105 110
 20 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
 115 120 125
 25 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
 130 135 140
 30 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
 145 150 155 160
 35 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
 165 170 175
 40 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
 180 185 190
 45 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
 195 200 205
 50 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
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 55 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
 225 230 235 240
 60 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
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 65 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 260 265 270
 70 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 275 280 285
 75 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
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 80 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
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 85 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 325 330 335
 90 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
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 95 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
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Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
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